# Online Appendix 16.A: Demonstration of Poisson sampling

This section illustrates Poisson sampling, understanding of which is needed to appreciate the radiological search model (RSM). The  parameter quantifies the distribution of the number of latent NLs per case. It is constrained to positive values.

#### Online Appendix 16.A.1: Code listing

#mainPoissonExample.R

rm(list = ls())

library(exactci)

K <- 100

lambdaP1 <- 1;lambdaP2 <- 2;

cat ("K = ", K,",

\nlambdaP 1st reader = ", lambdaP1,

"\nlambdaP 2nd reader = ", lambdaP2,"\n")

seed <- 1;set.seed(seed)

samples1 <- rpois(K,lambda = lambdaP1)

cat("obs. mean, reader 1 = ", mean(samples1), "\n")

seed <- 1;set.seed(seed)

samples2 <- rpois(K,lambda = lambdaP2)

cat("obs. mean, reader 2 = ", mean(samples2), "\n")

ret1 <- poisson.exact(sum(samples1),K)

ret2 <- poisson.exact(sum(samples2),K)

cat ("Rdr. 1: 95% CI = ", ret1$conf.int[1:2],"\n")

cat ("Rdr. 2: 95% CI = ", ret2$conf.int[1:2],"\n")

Note the usage of the R package exactci, for exact confidence intervals (these will generally be asymmetric and not include illegal values, like negative values for the Poisson parameter). If one gets a message like there is no package called ‘exactci’, it means the relevant package has not been loaded. Use the Packages – Install tabs in the lower right window of RStudio window to load the missing package.

Line 5 sets the number of samples K = 100. Line 6 initializes two values for : lambdaP1 = 1 and lambdaP2 = 2. Line 12 obtains K samples from a Poisson distribution with (population mean) parameter lambdaP1. The next line prints the mean of the samples. Lines 15 – 17 repeats these steps for lambdaP2.

Line 19 – 20 computes exact 95% confidence intervals for the observed means. The returned object is a list variable containing the confidence interval, as shown. Source the code to obtain book section 16.3.2.2.

As an exercise, the user should increase the number of samples by a factor of 100 and confirm that the width of each confidence interval decreases by a factor of 10. See book sections 16.3.2.3 and 16.3.2.4.

# Online Appendix 16.B: Demonstration of binomial sampling #1

This section illustrates Binomial sampling, understanding of which is needed to appreciate the radiological search model (RSM). The  parameter quantifies the distribution of the number of latent LLs per case. It is the probability that a lesion is actually found by the search mechanism.

#### Online Appendix 16.B.1: Code listing

#mainBinomialExample1.R

rm(list = ls())

library(exactci)

K2 <- 100;L <- 1;nuP1 <- 0.5;nuP2 <- 0.9;

cat ("K2 = ", K2,

"\nnuP 1st reader = ", 0.5,

"\nnuP 2nd reader = ", 0.9,"\n")

seed <- 1;set.seed(seed)

samples1 <- rbinom(K2,L,nuP1)

cat("mean, reader 1 = ", mean(samples1)/L, "\n")

seed <- 1;set.seed(seed)

samples2 <- rbinom(K2,L,nuP2)

cat("mean, reader 2 = ", mean(samples2)/L, "\n")

ret1 <- binom.exact(sum(samples1),K2\*L)

ret2 <- binom.exact(sum(samples2),K2\*L)

cat ("Rdr. 1: 95% CI = ", ret1$conf.int[1:2],"\n")

cat ("Rdr. 2: 95% CI = ", ret2$conf.int[1:2],"\n")

The number of samples, the number of lesions per case L, and the two values of (nuP1 and nuP2) are defined at line 5. Line 10 – 12 generates K2 binomial samples corresponding to trial size L = 1 (i.e., one lesion per diseased case) and success probability nuP1 and prints out the fraction of lesions found by the search mechanism. Line 14 – 16 repeats these steps for nuP2. The remaining lines calculate and print the 95% confidence intervals.

Question for reader: why is the number of samples denoted K in the Poisson case and K2 in the binomial case? Also, experiment with L = 2, 3, etc., and larger values of K2. The estimates approach the population values and the width of the confidence intervals shrink.

# Online Appendix 16.C: Demonstration of binomial sampling #2

The following is a more complicated but clinically more realistic example, where a dataset with 100 cases where 97 have one lesion per case, two have two lesions per case and one has three lesions per case, see line 5 in following code.

#### Online Appendix 16.C.1: Code listing

#mainBinomialExample2.R

rm(list = ls())

library(exactci)

K2 <- c(97,2,1);Lk <- c(1,2,3);nuP1 <- 0.5;nuP2 <- 0.9;

samples1 <- array(dim = c(sum(K2),length(K2)))

cat("K2[1] =", K2[1],

"\nK2[2] =", K2[2],

"\nK2[3] =", K2[3],

"\nnuP1 =", nuP1, "\nnuP2 =", nuP2, "\n")

seed <- 1;set.seed(seed)

for (l in 1:length(K2)) {

samples1[1:K2[l],l] <- rbinom(K2[l],Lk[l],nuP1)

}

cat("obsvd. mean, reader 1 = ",

sum(samples1[!is.na(samples1)])/sum(K2\*Lk), "\n")

samples2 <- array(dim = c(sum(K2),length(K2)))

seed <- 1;set.seed(seed)

for (l in 1:length(K2)) {

samples2[1:K2[l],l] <- rbinom(K2[l],Lk[l],nuP2)

}

cat("obsvd. mean, reader 2 = ",

sum(samples2[!is.na(samples2)])/sum(K2\*Lk), "\n")

ret1 <- binom.exact(sum(samples1[!is.na(samples1)]),sum(K2\*Lk))

ret2 <- binom.exact(sum(samples2[!is.na(samples2)]),sum(K2\*Lk))

cat ("Rdr. 1: 95% CI = ", ret1$conf.int[1:2],"\n")

cat ("Rdr. 2: 95% CI = ", ret2$conf.int[1:2],"\n")

Sourcing it yields book section 16.3.3.2.